



Fig.1

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Sequence information: *Saccharomyces cerevisiae* MFE-2 (SWISSPROT Q02207)
Length: 900 AA, Molecular weight: 98703 Da

10	20	30	40	50	60
MPGNLSFKDR	VVVITGAGGG	LGKVYALAYA	SRGAKVVVND	LG GTLGSGSH	NSKAADLVVD
70	80	90	100	110	120
EIKKAGGIAV	ANYDSVNENG	EKIIETAIKE	FGRVDVLINN	AGILRDVSFA	KMTEREFASV
130	140	150	160	170	180
VDVHLTGGYK	LSRAAWPYMR	SQKFGRIINT	ASPAGLFGNF	GQANYSAAKM	GLVGLAETLA
190	200	210	220	230	240
KEGAKYNINV	NSIAPLARSR	MTENVLPPII	LKQLGPEKIV	PLVLYLTHES	TKVNSISIFEL
250	260	270	280	290	300
AAGFFGQLRW	ERSSGQIFNP	DPKTYTPEAI	LNKWKETIDY	RDKPFNKTOH	PYQLSDYNDL
310	320	330	340	350	360
ITKAKKLPPN	EQGSVKIKSL	CNKVVVVVTA	GGGLGKSHAI	WFARYGAKVV	VNDIKDPFSV
370	380	390	400	410	420
VEEINKLYGE	GTAIPDSHDV	VTEAPLIQIT	AISKFORVDI	LVNNAGILRD	KSFLKMKDEE
430	440	450	460	470	480
WFAVLKVHLF	STFSLSKAVW	PIFTKQKSGF	IINTTSTSGI	YGNFGQANYA	AAKAAILGFS
490	500	510	520	530	540
KTIALEGAKR	GIIVNVIAPH	AETAMTKTIF	SEKELSNHFD	ASQVSPLVVL	LASEELQKYS
550	560	570	580	590	600
GRRVIGQLFE	VGGGWCQQTR	WQRSSGYVSI	KETIEPEEIK	ENWNHITDFS	RNTINPSSTE
610	620	630	640	650	660
ESSMATLQAV	QKAHSSKELD	DGLFKYTTKD	CILYNLGLGC	TSKELKYTYE	NDPDFQVLPT
670	680	690	700	710	720
FAVIPFMQAT	ATLAMDNLVD	NFNYAMLLHG	EQYFKLCTPT	MPSNGTLKTL	AKPLQVL DKN
730	740	750	760	770	780
GKAALVVGGF	ETYDIKTKKL	IAYNEG SFFI	RGAVPPEKE	VRD GKRKFA	VQNFEVPHGK
790	800	810	820	830	840
VPDFEAEIST	NKDQAALYRL	SGDFNPLHID	PTLAKAVKFP	TPILHGLCTL	GISAKALFEH
850	860	870	880	890	900
YGPYEELKVR	FTNVVFP GDT	LKV KAWKQGS	VVVFQTIDTT	RNVIVLDNAA	VKLSQAKSKL

Fig. 2

201020 06203007

Sequence information: *Saccharomyces cerevisiae* MFE-2 mutant A
 (G to S mutation at position 16)
 Length: 900 AA, Molecular weight: 98733 Da

10	20	30	40	50	60
MPGNLSFKDR	VVVITSAGGG	LGKVYALAYA	SRGAKVVVND	LGGTLGGSGH	NSKAADLVVD
70	80	90	100	110	120
EIKKAGGIAV	ANYDSVNENG	EKIIETAIKE	FGRVDVLINN	AGILRDVSFA	KMTEREFASV
130	140	150	160	170	180
VDVHLTGGYK	LSRAAWPYMR	SQKFGRRIINT	ASPAGLFGNF	GQANYSAAKM	GLVGLAETLA
190	200	210	220	230	240
KEGAKYNINV	NSIAPLARSR	MTENVLPPII	LKQLGPEKIV	PLVLYLTHES	TKVSNSIFEL
250	260	270	280	290	300
AAGFFGQLRW	ERSSGQIFNP	DPKTYTPEAI	LNKWKETIDY	RDKPFNKTQH	PYQLSDYNDL
310	320	330	340	350	360
ITKAKKLPPN	EQGSVKIKSL	CNKVVVVVGA	GGGLGKSHAI	WFARYGAKVV	VNDIKDPFSV
370	380	390	400	410	420
VEEINKLYGE	GTAIPDSHDV	VTEAPLIIQT	AISKFORVDI	LVNNAGILRD	KSFLKMKDEE
430	440	450	460	470	480
WFAVLKVHLF	STFSLSKAVW	PIFTKQKSGF	IINTTSTSGI	YGNFGQANYA	AKAAAILGFS
490	500	510	520	530	540
KTIALEGAKR	GIIVNVIAPI	AETAMTKTIF	SEKELSNHFD	ASQVSPVLVL	LASEELQKYS
550	560	570	580	590	600
GRRVIGQLFE	VGGGWCQQR	WQRSSGYVSI	KETIEPEEIK	ENWNHITDFS	RNTINPSSTE
610	620	630	640	650	660
ESSMATLQAV	QKAHSSKELD	DGLFKYTTKD	CILYNLGLGC	TSKELKYTYE	NDPDFQVLPT
670	680	690	700	710	720
FAVIPFMQAT	ATLAMDNLVD	NFNYAMLLHG	EQYFKLCTPT	MPSNGTLKTL	AKPLQVLKKN
730	740	750	760	770	780
GKAALVVGGF	ETYDIKTKKL	IAYNEGSFFI	RGAVPPEKE	VRDGKRAKFA	VQNFEVPHGK
790	800	810	820	830	840
VPDFEAEIST	NKDQAALYRL	SGDFNPLHID	PTLAKAVKFP	TPILHGLCTL	GISAKALFEH
850	860	870	880	890	900
YGPYEELKVR	FTNVVFPGDT	LKVKAWKQGS	VVVFQITDIT	RNVIVLDNAA	VKLSQAKSKL

Fig. 3

	10		20		30		40		50		60
	M	P	G	N	L	S	F	K	D	R	
	V	V	V	I	T	G	A	G	G	G	
	L	G	K	V	Y	A	L	A			
	S	R	G	A	K	V	V	N	D		
	L	G	G	T	L	G	G	S	G	H	
	N	S	K	A	A	D	L	V	D		
	70		80		90		100		110		120
	E	I	K	K	A	G	G	I	A	V	
	A	N	Y	D	S	V	N	E	N	G	
	E	K	I	I	E	T	A	I	K	E	
	F	G	R	V	D	V	L	I	N	N	
	A	G	I	L	R	D	V	S	F	A	
	K	M	T	E	R	E	F	A	S	V	
	130		140		150		160		170		180
	V	D	V	H	L	T	G	G	Y	K	
	L	S	R	A	A	W	P	Y	M	R	
	S	Q	K	F	G	R	I	I	N	T	
	A	S	P	A	G	L	F	G	N	F	
	G	Q	A	N	Y	S	A	A	K	M	
	G	L	V	G	L	A	E	T	L	A	
	190		200		210		220		230		240
	K	E	G	A	K	Y	N	I	N	V	
	N	S	I	A	P	L	A	R	S	R	
	M	T	E	N	V	L	P	P	H	I	
	L	K	Q	L	G	P	E	K	I	V	
	P	L	V	L	Y	L	T	H	E	S	
	T	K	V	S	N	S	I	F	E	L	
	250		260		270		280		290		300
	A	A	G	F	F	G	Q	L	R	W	
	E	R	S	S	G	Q	I	F	N	P	
	D	P	K	T	Y	T	P	E	A	I	
	L	N	K	W	K	E	I	T	D	Y	
	R	D	K	P	F	N	K	T	Q	H	
	P	Y	Q	L	S	D	I	N	D	L	
	310		320		330		340		350		360
	I	T	K	A	K	L	P	P	N		
	E	Q	G	S	V	K	I	K	S	L	
	C	N	K	V	V	V	T	S	A		
	G	G	G	L	G	K	S	H	A	I	
	W	F	A	R	Y	G	A	K	V	V	
	V	N	D	I	K	D	P	F	S	V	
	370		380		390		400		410		420
	V	E	E	I	N	K	L	Y	G	E	
	G	T	A	I	P	D	S	H	D	V	
	V	T	E	A	P	L	I	I	Q	T	
	A	I	S	K	F	Q	R	V	D	I	
	L	V	N	N	A	G	I	L	R	D	
	K	S	F	L	K	M	K	D	E	E	
	430		440		450		460		470		480
	W	F	A	V	L	K	V				

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Sequence information: *Saccharomyces cerevisiae* MFE-2 mutant A+B
(G to S mutation at position 16 and position 329)
Length: 900 AA, Molecular weight: 98763 Da

10	20	30	40	50	60
MPGNLSFKDR	VVVITSAGGG	LGKVYALAYA	SRGAKVVVND	LGGLTGGSGH	NSKAADLVVD
70	80	90	100	110	120
EIKKAGGIAV	ANYDSVNENG	EKIIETAIKE	FGRVDVLINN	AGILRDVSFA	KMTEREFASV
130	140	150	160	170	180
VDVHLTGQYK	LSRAAWPYMR	SQKFGRIINT	ASPAGLFGNF	GQANYSAAKM	GLVGLAETLA
190	200	210	220	230	240
KEGAKYNINV	NSIAPLARSR	MTENVLPPIH	LKQLGPEKIV	PLVLYLTHES	TKVSNSIFEL
250	260	270	280	290	300
AAGFFGQLRW	ERSSGQIFNP	DPKTYTPEAI	LNKWEITDY	RDKPFNKTQH	PYQLSDYNDL
310	320	330	340	350	360
ITKAKKLPPN	EQGSVKIKSL	CNKVVVVVTS	GGGLGKSHAI	WFARYGAKVV	VNDIKDPFSV
370	380	390	400	410	420
VEEINKLYGE	GTAIPDSHDV	VTEAPLIQIT	ASKFQRVDI	LVNNAGILRD	KSFLKMKDEE
430	440	450	460	470	480
WFAVLKVHLF	STFSLSKAVW	PIFTKQKSGF	IINTTSTSGI	YGNFGQANYA	AAKAAILGFS
490	500	510	520	530	540
KTIALEGAKR	GIIVNVIAPH	AETAMTKTIF	SEKELSNHFD	ASQVSPLVVL	LASEELQKYS
550	560	570	580	590	600
GRRVIGQLFE	VGGGWCGQTR	WQRSSGYVSI	KETIEPEEIK	ENWNHITDFS	RNTINPSSTE
610	620	630	640	650	660
ESSMATLQAV	QKAHSSKELD	DGLFKYTTKD	CILYNLGLGC	TSKELKYTYE	NDPDFQVLPT
670	680	690	700	710	720
FAVIPFMQAT	ATLAMDNLVD	NFNAYMLLHG	EQYFKLCTPT	MPSNGTLKTL	AKPLQVLDKN
730	740	750	760	770	780
GKAALVVGGF	ETYDIKTKKL	IAYNEGSFFI	RGAVPPEKE	VRDGKRAKFA	VQNFEVPHGK
790	800	810	820	830	840
VPDFEAEIST	NKDQAALYRL	SGDFNPLHID	PTLAKAVKFP	TPILHGLCTL	GISAKALFEH
850	860	870	880	890	900
YGPYEELKVR	FTNVVFPGDT	LKVKAWKQGS	VVVFQTIDTT	RNVIVLDNAA	VKLSQAKSKL

Fig. 5

10066230.020102

Variable	Mean	SD	Min	Max
Age	34.5	10.5	18	65
Gender	0.5	0.5	0	1
Marital status	0.5	0.5	0	1
Education	12.5	1.5	9	16
Income	15.5	5.5	10	25
Occupation	1.5	1.5	0	3
Health status	1.5	1.5	0	3
Stress level	2.5	1.5	0	4
Life satisfaction	3.5	1.5	1	5
Resilience	4.5	1.5	2	6
Optimism	3.5	1.5	1	5
Gratitude	4.5	1.5	2	6
Forgiveness	3.5	1.5	1	5
Empathy	4.5	1.5	2	6
Compassion	3.5	1.5	1	5
Kindness	4.5	1.5	2	6
Generosity	3.5	1.5	1	5
Patience	4.5	1.5	2	6
Self-control	3.5	1.5	1	5
Emotional stability	4.5	1.5	2	6
Psychological well-being	3.5	1.5	1	5
Life purpose	4.5	1.5	2	6
Meaning in life	3.5	1.5	1	5
Existential well-being	4.5	1.5	2	6
Transcendental well-being	3.5	1.5	1	5
Overall well-being	4.5	1.5	2	6

10	20	30	40	50	60
MSPVDFKDKV	VIITGAGGGL	GKYYSLEFAK	LGAKVVVNDL	GGALNGQGGN	SKAADVVVDE
70	80	90	100	110	120
IVKNGGVAVA	DYNNVLGDGK	IVETAVKNFG	TVHVIINNAG	ILRDASMKKM	TEKDYKLVID
130	140	150	160	170	180
VHLNGAFAVT	KAAPYFQKQ	KYGRIVNTSS	PAGLYGNFGQ	ANYASAKSAL	LGFAETLAKE
190	200	210	220	230	240
GAKYNIKANA	IAPLARSMT	ESILPPPMLE	KLGPEKVAPL	VLYLSSAENE	LTGQFFEVA
250	260	270	280	290	300
GFYAQIRWER	SGGVLFKPDQ	SFTAEEVAKR	FSEILDYDDS	RKPEYLNQY	PFMLNDYATL
310	320	330	340	350	360
TNEARKLPAN	DASGAPTVSL	KDKVVLITGA	GAGLGKEYAK	WFAKYGAKVV	VNDFKDATKT
370	380	390	400	410	420
VDEIKAAGGE	AWPDQHDVAK	DSEAIKNI	DKYGTIDILV	NNAGILRDRS	FAKMSKQEDW
430	440	450	460	470	480
SVQQVHLIGT	FNLSRLAWPY	FVEKQFGRII	NITSTSGIYG	NFGQANYSSS	KAGILGLSKT
490	500	510	520	530	540
MAIEGAKNNI	KVNIVAPHA	TAMTLTIFRE	QDKNLYHADQ	VAPLLVYLGT	DDVPVTGETF
550	560	570	580	590	600
EIGGGWIGNT	RWQRAKGAVS	HDEHTTVEFI	KEHLNEITDF	TTDTENPKST	TESSMAILSA
610	620	630	640	650	660
VGGDDDDDE	DEEEDGDEE	EDEEDEEEDD	PVWRFDDRDV	ILYNIALGAT	TKQLKYVYEN
670	680	690	700	710	720
DSDFQVIPTF	GHLITFNSGK	SQNSFAKLLR	NFNPMLLLHG	EHYLVHNSWP	PPTEGEIKTT
730	740	750	760	770	780
FEPIATTPKG	TNVVIVHGSK	SVDNKSGLI	YSNEATYFIR	NCQADNKVYA	DRPAPATNQF
790	800	810	820	830	840
LAPKRAPDYQ	VDVPVSEDLA	ALYRLSGDRN	PLHIDPNFAK	GAKFPKPILH	GMCTYGLSAK
850	860	870	880	890	900
ALIDKFGMFN	EIKARFTGIV	FPGETLRVLA	WKESDDTIVF	QTHVVDRGTI	AINNAAIKLV
906					
GDKAKI					

Fig. 6

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Sequence information: *Candida tropicalis* MFE-2 mutant A
(G to S mutation in position 15)
Length: 906 AA, Molecular weight: 99499 Da

10	20	30	40	50	60
MSPVDFKDKV	VIITSAGGGL	GKYYSLEFAK	LGAKVVVNDL	GGALNGQGGN	SKAADVVVDE
70	80	90	100	110	120
IVKNGGVAVA	DYNNVLDGDK	IVETAVKNFG	TVHVIINNAG	ILRDASMKKM	TEKDYLKVID
130	140	150	160	170	180
VHLNGAFVAVT	KAAPYFQKQ	KYGRIVNTSS	PAGLYGNFGQ	ANYASAKSAL	LGFAETLAKE
190	200	210	220	230	240
GAKYNIKANA	IAPLARSMT	ESILPPPMLE	KLGPKEVAPL	VLYLSSAENE	LTGQFFEVA
250	260	270	280	290	300
GFYAQIRWER	SGGVLFKPDQ	SFTAEEVAKR	FSEILDYDDS	RKPEYLKNQY	PFMLNDYATL
310	320	330	340	350	360
TNEARKLPAN	DASGAPTIVSL	KDKVVLITGA	GAGLGKEYAK	WFAKYGAKVV	VNDFKDATKT
370	380	390	400	410	420
VDEIKAAGGE	AWPDQHDVAK	DSEAIKNVI	DKYGTIDILV	NNAGILRDRS	FAKMSKQEW
430	440	450	460	470	480
SVQQVHLIGT	FNLRLAWPY	FVEKQFGRII	NITSTSGIYG	NFGQANYSSS	KAGILGLSKT
490	500	510	520	530	540
MAIEGAKNNI	KVNIVAPHA	TAMTLTIFRE	QDKNLYHADQ	VAPLLVYLGT	DDVPVTGETF
550	560	570	580	590	600
EIGGGWIGNT	RWQRAKAVS	HDEHTTVEFI	KEHLNEITDF	TTDTENPKST	TESSMAILSA
610	620	630	640	650	660
VGGDDDDDE	DEEEDGDEE	EDEEDEEED	PVWRFDNRDV	ILYNIALGAT	TKQLKYVYEN
670	680	690	700	710	720
DSDFQVIPTF	GHLITFNSGK	SQNSFAKLLR	NFNPMLLLHG	EHYLVHNSWP	PPTEGEIKTT
730	740	750	760	770	780
FEPIATTPKG	TNVVIVHGSK	SVDNKGELI	YSNEATYFIR	NCQADNKVYA	DRPAFATNQF
790	800	810	820	830	840
LAPKRADPYQ	VDVPVSEDLA	ALYRLSGDRN	PLHIDPNFAK	GAKFPKPILH	GMCTYGLSAK
850	860	870	880	890	900
ALIDKFGMFN	EIKARFTGIV	FPGETLRVLA	WKESDDTIVF	QTHVVDRGTI	AINNAAIKLV
906					
GDKAKI					

Fig. 7

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Sequence information: *Candida tropicalis* MFE-2 mutant B
(G to S mutation in position 329)
Length: 906 AA, Molecular weight: 99499 Da

10	20	30	40	50	60
MSPVDFKDKV	VIITGAGGGL	GKYYSLFAK	LGAKVVVNDL	GGALNGQGGN	SKAADVVVDE
70	80	90	100	110	120
IVKNGGVAVA	DYNNVLDGDK	IVETAVKNFG	TVHVIINNAG	ILRDASMKKM	TEKDYKLVID
130	140	150	160	170	180
VHLNGAFAVT	KAAPYFQKQ	KYGRIVNTSS	PAGLYGNFGQ	ANYASAKSAL	LGFAETLAKE
190	200	210	220	230	240
GAKYNIKANA	IAPLARSMT	ESILPPPMLE	KLGPVKVAPL	VLYLSSAENE	LTGQFFEVA
250	260	270	280	290	300
GFYAQIRWER	SGGVLFKPDQ	SFTAEEVAKR	FSEILDYDDS	RKPEYLKNQY	PFMLNDYATL
310	320	330	340	350	360
TNEARKLPAN	DASGAPTIVSL	KDKVVLITSA	GAGLGKEYAK	WFAKYGAKVV	VNDFKDATKT
370	380	390	400	410	420
VDEIKAAGGE	AWPDQHDVAK	DSEAIKNI	DKYGTIDILV	NNAGILRDRS	FAKMSKQEW
430	440	450	460	470	480
SVQQVHLIGT	FNLSRLAWPY	FVEKQFGRII	NITSTSGIYG	NFGQANYSSS	KAGILGLSKT
490	500	510	520	530	540
MAIEGAKNNI	KVNIVAPHAE	TAMTLTIFRE	QDKNLYHADQ	VAPLLVYLGT	DDVPVTGETF
550	560	570	580	590	600
EIGGGWIGNT	RWQRAKGAVS	HDEHTTVEFI	KEHLNEITDF	TTDTENPKST	TESSMAILSA
610	620	630	640	650	660
VGGDDDDDE	DEEEDGDEE	EDEEDEEDD	PVWRFDDR	ILYNIALGAT	TKQLKYVYEN
670	680	690	700	710	720
DSDFQVIPTF	GHLITFNSGK	SQNSFAKLLR	NFNPMLLLHG	EHYLVHNSWP	PPTEGEIKTT
730	740	750	760	770	780
FEPIATTPKG	TNVVIVHGSK	SVDNKGELI	YSNEATYFIR	NCQADNKVYA	DRPAFATNQF
790	800	810	820	830	840
LAPKRAPDYQ	VDVPVSEDLA	ALYRLSGDRN	PLHIDPNFAK	GAKFPKPILH	GMCTYGLSAK
850	860	870	880	890	900
ALIDKFGMFN	EIKARFTGIV	FPGETLRVLA	WKESDDTIVF	QTHVVDRGTI	AINNAAIKLV
906					
GDKAKI					

Fig. 8

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Sequence information: *Candida tropicalis* MFE-2 mutant A+B
(G to S mutation in position 15 and position 329)
Length: 906 AA, Molecular weight: 99529 Da

10	20	30	40	50	60
MSPVDFKDKV	VIITSAGGGL	GKYYSLEFAK	LGAKVVVNDL	GGALNGQGGN	SKAADVVVDE
70	80	90	100	110	120
IVKNGGVAVA	DYNNVLDGDK	IVETAVKNFG	TVHVIINNAG	ILRDASMKKM	TEKDYKLVID
130	140	150	160	170	180
VHLNGAFAVT	KAAWPFYQKQ	KYGRIVNTSS	PAGLYGNFGQ	ANYASAKSAL	LGFAETLAKE
190	200	210	220	230	240
GAKYNIKANA	IAPLARSRMT	ESILPPPMLE	KLGPKEKVAPL	VLYLSSAENE	LTGQFFEVA
250	260	270	280	290	300
GFYAQIRWER	SGGVLFKPDQ	SFTAENVAKR	FSEILDYDDS	RKPEYLKNQY	PFMLNDYATL
310	320	330	340	350	360
TNEARKLPAN	DASGAPTVSL	KDKVVLITSA	GAGLGKEYAK	WFAKYGAKVV	VNDFKDATKT
370	380	390	400	410	420
VDEIKAAGGE	AWPDQHDVAK	DSEAIKKNVI	DKYGTIDILV	NNAGILRDRS	FAKMSKQEW
430	440	450	460	470	480
SVQQVHLIGT	FNLSRLAWPY	FVEKQFGRII	NITSTSGIYG	NFGQANYSSS	KAGILGLSKT
490	500	510	520	530	540
MAIEGAKNNI	KVNIVAPHA	TAMTLTIFRE	QDKNLYHADQ	VAPLLVYLGT	DDVPVTGETF
550	560	570	580	590	600
EIGGGWIGNT	RWQRAKGAVS	HDEHTTVEFI	KEHLNEITDF	TTDTENPKST	TESSMAILSA
610	620	630	640	650	660
VGGDDDDDE	DEEEDGDEE	EDEEDEEDD	PVWRFDDRDV	ILYNIALGAT	TKQLKYVYEN
670	680	690	700	710	720
DSDFQVIPTF	GHLITFNSGK	SQNSFAKLLR	NFNPMLLLHG	EHYLVHSWP	PTTEGEIKTT
730	740	750	760	770	780
FEPIATTFKG	TNVVIVHGSK	SVDNKGELI	YSNEATYFIR	NCQADNKVYA	DRPAFATNQF
790	800	810	820	830	840
LAPKRAPDYQ	VDVPVSEDLA	ALYRLSGDRN	PLHIDPNFAK	GAKFPKPILH	GMCTYGLSAK
850	860	870	880	890	900
ALIDKFGMFN	EIKARFTGIV	FPGETLRVLA	WKESDDTIVF	QTHVVDRGTI	AINNAAIKLV
906					
GDKAKI					

Fig. 9

10060230.020402

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Sequence information: human 17-beta-hydroxysteroid dehydrogenase 4
(SWISSPROT P51659) (same protein as human MFE-2)
Length: 736 AA, Molecular weight: 79686 Da

10	20	30	40	50	60
MGSP	LRFDGR	VVLVTGAGAG	LGRAYALAF	ER	GALVVVND
LGGDFKGVGK					
GSLAADKVVE					
70	80	90	100	110	120
EIRRR	GGKAV	ANYDSVEEGE	KVVK	TALDAF	GRIDVVV
NNA					
GILRDRSFAR					
ISDEDWDIIH					
130	140	150	160	170	180
RVHLR	GSFQV	TRAAWEHMKK	QKYGRIIMTS	SASGIYGNFG	QANYSAAKLG
LLGLANSLAI					
190	200	210	220	230	240
EGRKS	NIHCN	TIAPNAGSRM	TQTVMPEDLV	EALKPEYVAP	LVLWLCHESC
EENGGLFEVG					
250	260	270	280	290	300
AGWIG	KLRWE	RTLGAIVRQK	NHPMTPEAVK	ANWKKICDFE	NASKPQSIQE
STGSIIEVLS					
310	320	330	340	350	360
KIDSE	GGVSA	NHTSRATSTA	TSGFAGAIGQ	KLPPFSYAYT	ELEAIMYALG
VGASIKDPKD					
370	380	390	400	410	420
LKFIY	EGSSD	FSCLPTFGVI	IGQKSMGGG	LAEIPGLSIN	FAKVLHGEQY
LELYKPLPRA					
430	440	450	460	470	480
GKLK	CEAVVA	DVLDKGSGVV	IIMDVYSYSE	KELICHNQFS	LFLVGSGGFG
GKRTSDKVKV					
490	500	510	520	530	540
AVAIP	NRPPD	AVLTDTTSLN	QAALYRLSGD	WNPLHIDPNF	ASLAGFDKPI
LHGLCTFGFS					
550	560	570	580	590	600
ARRVL	QQFAD	NDVSRFKAIAK	ARFAKPVYPG	QTLQTEMWKE	GNRIHFQTKV
QETGDIVISN					
610	620	630	640	650	660
AYVDL	APTSG	TSAKTPSEGG	KLQSTFVFEE	IGRRLKDIGP	EVVKKVNAVF
EWHITKGGNI					
670	680	690	700	710	720
GAKWT	IDLKS	GSGKVYQGPA	KGAADTTIIL	SDEDFMEVVL	GKLDPQKAFF
SGRLKARGNI					
730	736				
MLSQ	KLQMIL	KDYAKL			

Fig. 10

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Sequence information: human 17-beta-hydroxysteroid dehydrogenase 4
mutant (G to S mutation at position 16)
Length: 736 AA, Molecular weight: 79686 Da

10	20	30	40	50	60			
MGSP	LRFDGR	VVLVTSAGAG	LGRAYALAF	ER	GALVVVND	LGGDFKGVGK	GSLAADKVVE	
70	80	90	100	110	120			
EIRRRG	GKAV	ANYDSVEEGE	KVVK	TALDAF	GRIDVVV	NA	GILRDRSFAR	ISDEDWDIIH
130	140	150	160	170	180			
RVHLRG	SFQV	TRAAWEHMKK	QKYGRIIMTS	SASGIYGNFG	QANYSAAKLG	LLGLANSLAI		
190	200	210	220	230	240			
EGRKSN	IHCHN	TIAPNAGSRM	TQTVMPEDIV	EALKPEYVAP	LVLWLCHESC	EENGGLFEVG		
250	260	270	280	290	300			
AGWIGK	LRWE	RTLGAIVRQK	NHPMTPEAVK	ANWKKICDFE	NASKPQSIQE	STGSIIEVLS		
310	320	330	340	350	360			
KIDSEGG	VSA	NHTSRATSTA	TSGFAGAIGQ	KLPPFSYAYT	ELEAIMYALG	VGASIKDPKD		
370	380	390	400	410	420			
LKFIYEG	SSD	FSCLPTFGVI	IGQKSMGGG	LAEIPGLSIN	FAKVLHGEQY	LELYKPLPRA		
430	440	450	460	470	480			
GKLKCEA	VVA	DVLDKGSGVV	IIMDVYSYSE	KELICHNQFS	LFLVGSGGFG	GKRTSDKVKV		
490	500	510	520	530	540			
AVAIPNR	PPD	AVLTDTTSLN	QAALYRLSGD	WNPLHIDPNF	ASLAGFDKPI	LHGLCTFGFS		
550	560	570	580	590	600			
ARRVLQ	QFAD	NDVSRFKA	IK	ARFAKPVYPG	QTLQTEMWKE	GNRIHFQTKV	QETGDIVISN	
610	620	630	640	650	660			
AYVDLAP	TSG	TSAKTPSEGG	KLQSTFVFEE	IGRRLKDIGP	EVVKKVN	AVF	EWGITKGGNI	
670	680	690	700	710	720			
GAKWTID	LKS	GSGKVYQGPA	KGAADTTIIL	SDEDFMEVVL	GKLDPQK	AFF	SGRLKARGNI	
730	736							
MLSQKLQ	MIL	KDYAKL						

Fig. 11

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